--Figure 10 (SEQ ID NO: 5) shows a comparison of the predicted translated product of a *Brassica napus FLF-like* sequence (top lines), and the predicted *FLF* translation product from *Arabidopsis thaliana*, showing identical amino acids (|), highly conserved amino acids (:) and conserved amino acids (.).--

Please replace the first paragraph on page 44 of with the following rewritten paragraph in its place.

--The cDNA sequences and predicted amino acid sequences are set out in SEQ ID NOS: 6 to 15 and SEQ ID NOS: 16 to 25 respectively. The sequences probably represent 5 genes, grouped as follows:

12.1/16.1

15.1/16.2/18.2

11.2

14.1/18.1/20.1

11.3

The partial genomic sequence and translation in Figure 9 correspond to the cDNAs 12.1/16.1.--

Please replace the first paragraph of Example 5 on page 22 with the following rewritten paragraph in its place.

--Example 5 Construction of 35S::gene A plasmid

As the larger of the initially isolated gene A cDNA clones lacked the AT of the ATG of the start codon, oligonucleotide-directed mutagenesis was employed to generate a 200bp

fragment from the 5' end of the cDNA which contained the absent nucleotides. Two oligonucleotides were synthesized on an Applied Biosystems DNA Synthesizer for this purpose:-

(1) (SEQ ID NO: 31)

5' AAG**CCGCGG**ACAATGGAAGCTGTAAGATGC 3'

(2) (SEQ ID NO: 32)

5' GAGAGGCTG**GTTAAC**CGGAG 3'.--

Please replace Example 6 on page 23 with the following rewritten example in its place.

--Example 6 Construction of 35S::gene B plasmid

A binary construct containing gene B under the control of the CaMV 35S promoter was generated by cloning a XhoI/SpeI digested PCR product, amplified using the gene B cDNA clone as template with the primers, using methods similar to those described in Example 5:

(SEQ ID NO: 33) 5' CCG**CTCGAG**CTTAGTATCTCCGGCG 3' and

(SEQ ID NO: 34) 5' GG**ACTAGT**CGCCCTTATCAGCGGA 3',

in which restriction sites are shown in bold, and the sequence hybridizing to gene B cDNA is underlined, into XhoI/SpeI digested pART7 (Gleaves, 1992) containing the CaMV 35S promoter. The 35S::gene B cassette was then subcloned using NotI into pART27 (Gleaves, 1992) and introduced into *A. tumefaciens* strain GV3101 (Koncz and Schell, 1986) as described above. Transgenic plants were generated by *in planta* transformation (Bechthold et al, 1993).--

Please replace the first full paragraph on page 24 (part of Example 7) with the

following rewritten paragraph in its place.

--The NPTII probe was generated as described above. The 3' Ac probe was a SphI fragment (Lawrence *et al*, 1993), and probe 4 was generated by amplification of the wild-type genomic clone with primers:

(SEQ ID NO: 35) 5' -GTATAGGGCACATGCCC-3' and

(SEQ ID NO: 36) 5' -CACTCGGAGCTGTGCC-3'.--

Please replace the first paragraph of Example 13 on page 30 with the following rewritten paragraph in its place.

--Example 13 Anti-Sense Constructs

Anti-sense plant constructs have been generated using an anti-sense *FLF* gene construct under the control of the CaMV 35S promoter. A 35S::*FLF* antisense binary construct was generated by cloning the EcoRI/SpeI digested PCR product amplified with primers

(SEQ ID NO: 37) CG**GAATTC**TCACACGAATAAGGTAC and

(SEQ ID NO: 38) GG**ACTAGT**GGTCAAGATCCTTGATC

as described for the 35S::*FLF* construct. This amplified the region downstream of the MADS box, so that the antisense construct lacks the MADS box region. The PCR product was cloned into pART7 and pBART 27 (which is a derivative of pART27), and transgenic plants were generated as described above, except that the *Bar* gene was used as the selectable marker.--

Please replace the first full paragraph on page 43 with the following rewritten paragraph in its place.

--The partial genomic sequence of the *Brassica napus FLF-like* gene is set out in SEQ ID NO. 4 (Figure 9), and the amino acid sequence of the predicted translation product is set out in SEQ ID NO. 5 (Figure 10). The partial genomic sequence, showing the location of exons and the sequence of the corresponding translated product, is illustrated in Figure 9, and the sequence of the predicted translated product from the *Brassica napus* gene is compared with the corresponding product from *Arabidopsis thaliana FLF* in Figure 10. There is a high degree of conservation, with 79% identity and 83% similarity in the deduced FLF protein sequence (as determined by the University of Wisconsin Genetics Computer Group software package version 9.1, using default parameters).--

Please replace the second paragraph on page 51 (continuing onto page 52) with the following rewritten paragraph in its place.

--cDNA from a chromosome 1 *FLF* –like gene (*FLF-LIKE1*) was isolated using a RT PCR based method. First strand cDNA was generated from 5 μg of Col-0 total RNA. Reactions were carried out using Superscript II (GIBCO BRL) in a 20 μl volume according to the manufacturer's instructions. *FLF-LIKE1* transcript was amplified by PCR using 1μl of the first strand cDNA synthesis reaction as template with primers :

(SEQ ID NO: 39) 5'-ATTGAATTCGGGCATAACCCTTATCGGAGATTTG-3' and

(SEQ ID NO: 40) 5'-AACGGATCCGTTGATGATGGTGGCTAATTGAGCAG-3';

Eco RI and Bam HI restriction sites respectively are underlined. The amplification reaction was carried out in a final volume of 40 μl, which contained 2.5 μM of each oligonucleotide primer, 1.0 units of Amplitaq Polymerase (Perkin Elmer) and 250 μM of each of the four deoxynucleotides. Conditions for amplification were as follows: 94°C for 2 min, 40 cycles

consisting of 15 s denaturation at 94°C, annealing at 55°C for 15 s and polymerisation at 72°C for 1 min, and a final extension at 72°C for 4 min before the temperature was decreased to 25°C. PCR products were purified using QIAquick PCR purification kit (Qiagen), digested with restriction enzymes Eco RI/Bam HI, and ligated into the corresponding restriction sites of a pBIISK+ vector (Stratagene). Positive colonies were sequenced using universal primers with the Applied Biosystems Big Dye terminator sequencing mix according to the manufacturer's instructions, and analysed using an Applied Biosystems 377 sequencing machine (Perkin Elmer). cDNA sequences obtained were compared to *Arabidopsis* genomic sequence (BAC F22K20; AC002291). The University of Wisconsin GCG software package was employed for sequence analysis.--

Please replace the second paragraph on page 52 with the following rewritten paragraph in its place.

--A binary construct containing the *FLF-LIKE1* cDNA under the control of a *CaMV 35S* promoter was generated by cloning an Eco RI/Kpn I digested PCR product into an Eco RI/Kpn I pART7 vector (Gleave, 1992) containing a *CaMV 35S* promoter. The PCR product was amplified using 200 pg of the *FLF-LIKE1* cDNA clone as template with primers:

(SEQ ID NO: 41) 5'-ATTGAATTCGGGCATAACCCTTATCGGAGATTTG-3' and

(SEQ ID NO: 42) 5'-CTAGTGGTACCGTTGATGATGGTGGCTAATTGAGC-3';

Eco RI and Kpn I restriction sites respectively are underlined. The amplification reaction was carried out as described above. The cloned PCR product was sequenced to ensure that no mutations had been introduced during the amplification procedure. The *35S::FLF-LIKE1* cassette was then subcloned into pART27 using Not I (Gleave, 1992), and introduced into